

C. W.

## RAW SEQUENCE LISTING ERROR REPORT

BIOLOGY  
SYSTEMS  
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/445,174

Source: 1655

Date Processed by STIC: 7-26-00

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JUL 16  
CENTEX 1000/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY  
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT  
COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY  
or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,  
WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,  
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/445, 174

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos  
The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length  
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering  
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII  
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length  
Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)  
Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)  
Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)  
Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES)  
Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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AUG 16 2003

TECH CENTER 160Q/2900

1655

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000  
 TIME: 10:17:06

Input Set : A:\115541\_1.txt  
 Output Set: N:\CRF3\07262000\I445174.raw

Does Not Comply  
 Corrected Diskette Needed

1 <110> APPLICANT: van Ommen, Garrit J.B.  
 2 Petrij-Bosch, Anne  
 3 Bakker, Egbert  
 4 Devilee, Peter  
 7 <120> TITLE OF INVENTION: A diagnostic test kit for determining a predisposition  
 8 for breast and ovarian cancer, materials and methods  
 9 for such determination  
 11 <130> FILE REFERENCE: P22163CA00  
 13 <140> CURRENT APPLICATION NUMBER: US 09/445,174  
 14 <141> CURRENT FILING DATE: 2000-04-24  
 16 <150> PRIOR APPLICATION NUMBER: PCT/NL98/00325  
 17 <151> PRIOR FILING DATE: 1998-06-03  
 19 <150> PRIOR APPLICATION NUMBER: EP 97201700.8  
 20 <151> PRIOR FILING DATE: 1997-06-04  
 22 <160> NUMBER OF SEQ ID NOS: 23  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 20  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Artificial Sequence  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward  
 33 for D17S1322  
 35 <400> SEQUENCE: 1  
 36 ctgacctggg caacaaacga 20  
 39 <210> SEQ ID NO: 2  
 40 <211> LENGTH: 20  
 41 <212> TYPE: DNA  
 42 <213> ORGANISM: Artificial Sequence  
 44 <220> FEATURE:  
 45 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse  
 46 for D17S1322  
 48 <400> SEQUENCE: 2  
 49 gcaggaagca ggaatggaac 20  
 52 <210> SEQ ID NO: 3  
 53 <211> LENGTH: 21  
 54 <212> TYPE: DNA  
 55 <213> ORGANISM: Artificial Sequence  
 57 <220> FEATURE:  
 58 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward  
 59 for D17S855  
 61 <400> SEQUENCE: 3  
 62 ggatggcctt ttagaaagtg g 21  
 65 <210> SEQ ID NO: 4  
 66 <211> LENGTH: 20  
 67 <212> TYPE: DNA  
 68 <213> ORGANISM: Artificial Sequence

See p. 5

RAW SEQUENCE LISTING                      DATE: 07/26/2000  
 PATENT APPLICATION: US/09/445,174        TIME: 10:17:06

Input Set : A:\115541\_1.txt  
 Output Set: N:\CRF3\07262000\I445174.raw

```

70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
72   for D17S855
74 <400> SEQUENCE: 4
75 acacagactt gtcctactgc .                20
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 20
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
85   for D17S1323
87 <400> SEQUENCE: 5
88 taggagatgg attattggtg                20
91 <210> SEQ ID NO: 6
92 <211> LENGTH: 20
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
98   for D17S1323
100 <400> SEQUENCE: 6
101 aagcaacttt gcaatgagtg                20
104 <210> SEQ ID NO: 7
105 <211> LENGTH: 22
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
111   for first PCR
113 <400> SEQUENCE: 7
114 tcacagtgca gtgaattgga ag            22
117 <210> SEQ ID NO: 8
118 <211> LENGTH: 24
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
124   for first PCR
126 <400> SEQUENCE: 8
127 gtagccagga cagtagaagg actg          24
130 <210> SEQ ID NO: 9
131 <211> LENGTH: 22
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
137   for second PCR
139 <400> SEQUENCE: 9

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000  
 TIME: 10:17:06

Input Set : A:\115541\_1.txt  
 Output Set: N:\CRF3\07262000\I445174.raw

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140 gaagaaagag gaacgggctt gg                                22
143 <210> SEQ ID NO: 10
144 <211> LENGTH: 21
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
150     for second PCR
152 <400> SEQUENCE: 10
153 ggcactttg taagctcatt c                                21
156 <210> SEQ ID NO: 11
157 <211> LENGTH: 19
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
164 <400> SEQUENCE: 11
165 aaccaccaag gtccaaagc                                19
168 <210> SEQ ID NO: 12
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
176 <400> SEQUENCE: 12
177 gtagccagga cagtagaagg actg                            24
180 <210> SEQ ID NO: 13
181 <211> LENGTH: 20
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
188 <400> SEQUENCE: 13
189 tacgtgggtt caactgaagc                                20
192 <210> SEQ ID NO: 14
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward
200 <400> SEQUENCE: 14
201 tccattgag aggtcttgct                                20
204 <210> SEQ ID NO: 15
205 <211> LENGTH: 20
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse
212 <400> SEQUENCE: 15

```

## RAW SEQUENCE LISTING

DATE: 07/26/2000

PATENT APPLICATION: US/09/445,174

TIME: 10:17:06

Input Set : A:\115541\_1.txt

Output Set: N:\CRF3\07262000\I445174.raw

```

213 actgtgctac tcaagcacca                20
216 <210> SEQ ID NO: 16
217 <211> LENGTH: 24
218 <212> TYPE: DNA ✓
219 <213> ORGANISM: Artificial Sequence ✓
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward ✓
224 <400> SEQUENCE: 16
225 gaaaaaaaaag tacaaccaa tgcc                24
228 <210> SEQ ID NO: 17
229 <211> LENGTH: 24
230 <212> TYPE: DNA ✓
231 <213> ORGANISM: Artificial Sequence ✓
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse ✓
236 <400> SEQUENCE: 17
237 agcccacttc attagtactg gaac                24
240 <210> SEQ ID NO: 18
241 <211> LENGTH: 24
242 <212> TYPE: DNA ✓
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: primer forward ✓
248 <400> SEQUENCE: 18
249 taccctataa gccagaatcc agaa                24
252 <210> SEQ ID NO: 19
253 <211> LENGTH: 21
254 <212> TYPE: DNA ✓
255 <213> ORGANISM: Artificial Sequence ✓
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: primer reverse ✓
260 <400> SEQUENCE: 19
261 ggccactttg taagtcatt c                21
264 <210> SEQ ID NO: 20
265 <211> LENGTH: 720
266 <212> TYPE: DNA ✓
267 <213> ORGANISM: Homo sapiens ✓
269 <220> FEATURE:
270 <223> OTHER INFORMATION: /note="Exon 22 of BRCA1 and its flanking intron
271 sequences, pos. 79441-80160"
273 <400> SEQUENCE: 20
274 agaggtcttg ctataagcct tcatccggag agtgtagggt agagggcctg ggttaagtat 60
275 gcagattact gcagtgattt tacatctaaa tgtccatttt agatcaactg gaatggatgg 120
276 tacagctgtg tgggtcttct gtggtgaagg agctttcattc attcaccctt ggcacagtaa 180
277 gtattgggtg ccctgtcaga gagggaggac acaatattct ctctgtgtgag caagactggc 240
278 acctgtcagt ccctatggat gccctactg tagcctcaga agtcttctct gccacatac 300
279 ctgtgccaaa agactccatc tgtaagggat gggtaaggat ttgagaactg cacatattaa 360
280 atatactgag ggaagacttt ttccctctaa ctctttttcc catatgtccc tccccctcct 420
281 ctctgtgact gcccagcat actgtgtttc aacaaatcat caagaaatga tgggctggag 480

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000  
TIME: 10:17:06

Input Set : A:\115541\_1.txt  
Output Set: N:\CRF3\07262000\I445174.raw

```

282 gctgggcatg gtggctcatg tctgtaatcc cagcactttg ggaggccgag gcagggtggat 540
283 cacttgtagc gagtttgaga ccagcctggc caacatggtg aaaccccatc tgtactaaaa 600
284 aaaaaaaaaa aaaaagtagc caggcctggt ggagcatgcc tgtaatgcca gctatttggg 660
285 aagttgaggt gtgagcatcg cttgaacgtg ggaggcagag gttgcagtga gccaaagattg 720
288 <210> SEQ ID NO: 21
289 <211> LENGTH: 180
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <223> OTHER INFORMATION: /note="Intronic region flanking exon 12, pos.
295 44423 - 44600"
297 <400> SEQUENCE: 21
W--> 298 cctgtaatcc cagcactttg ggaggccgag gcgggaggat catgtgⓈ caggagatcc 60
299 agaccatcct ggctaacacg gtgaaacacc atttctacta aaactacaaa aaattagctg 120
300 ggcatggtgg cgggcgctg taatcccagc tactcaggag gctgaagcag aagaatggct 180
303 <210> SEQ ID NO: 22
304 <211> LENGTH: 180
305 <212> TYPE: DNA
306 <213> ORGANISM: Homo sapiens
308 <220> FEATURE:
309 <223> OTHER INFORMATION: /note="Intronic region flanking exon 13, pos.
310 48256 - 48436"
312 <400> SEQUENCE: 22
313 cctgtaaccc cagcactttg ggaggccaag gcaggcgaat cacctgaggt cgggagctcg 60
314 agaccagcct gaccaacatg gagaaaccac atctctacta aaactacaaa aaattagccg 120
315 ggcggtggtg cacatgcctg taatcccagc tacttgggag ctacggtgcc tggcctagtt 180
318 <210> SEQ ID NO: 23
319 <211> LENGTH: 60
320 <212> TYPE: DNA
321 <213> ORGANISM: Homo sapiens
323 <220> FEATURE:
324 <223> OTHER INFORMATION: /note="Deletion-function fragment"
326 <400> SEQUENCE: 23
327 agaccatcct ggctaacacg gtgaaacacc atttctacta aaactacaaa aaattagccg 60

```

*Mandatory features missing  
<221> <222> <223>  
Explain location of  
n's and residues  
they represent.  
See # 10 on  
Error Summary  
Sheet.*

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AUG 16 2000  
TECH CENTER 1600/2000

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/445,174

DATE: 07/26/2000

TIME: 10:17:07

Input Set : A:\115541\_1.txt

Output Set: N:\CRF3\07262000\I445174.raw

L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21  
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
L:298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21

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